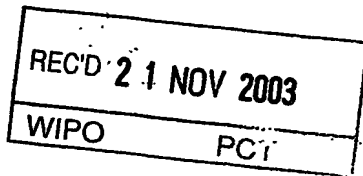




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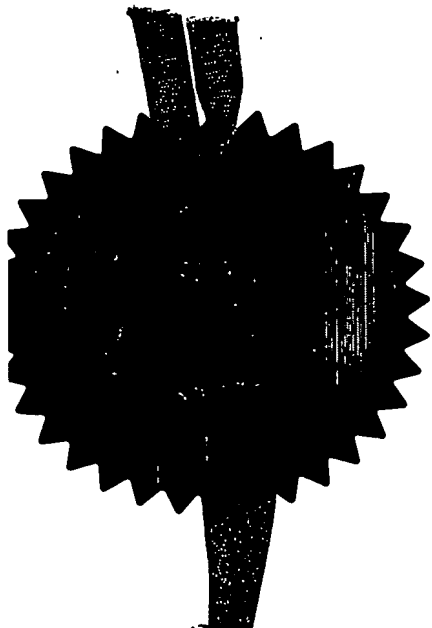
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Request for grant of a patent

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1. Your reference	444.78613/000		
2. Patent application number (The Patent Office will fill in this part)	0225550.3		
3. Full name, address and postcode of the or of each applicant (underline all surnames)	Bioparken AS Fredrik A Dahls vei 20 N-1432 Ås Norway		
Patents ADP number (if you know it)			
If the applicant is a corporate body, give country/state of incorporation	Norway		
4. Title of the invention	ASSAY		
5. Name of your agent (if you have one)	Frank B. Dehn & Co.		
"Address for service" in the United Kingdom to which all correspondence should be sent (including the postcode)	179 Queen Victoria Street London EC4V 4EL		
Patents ADP number (if you know it)	166001		
6. If you are declaring priority from one or more earlier patent applications, give the country and the date of filing of the or of each of these earlier applications and (if you know it) the or each application number	Country	Priority application number (if you know it)	Date of filing (day / month / year)
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8. Is a statement of inventorship and of right to grant of a patent required in support of this request? (Answer 'Yes' if: a) any applicant named in part 3 is not an inventor, or b) there is an inventor who is not named as an applicant, or c) any named applicant is a corporate body. See note (d))	Yes		

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Priority documents -

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Statement of inventorship and right to grant of a patent (Patents Form 7/77) -

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11. I/We request the grant of a patent on the basis of this application.

Signature Date 1st November 2002
Frank B Dehn & Co

12. Name and daytime telephone number of person to contact in the United Kingdom

Julian Cockbain
020 7206 0600

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Assay

5 This invention relates to an assay method for
detecting fungal infection of fields, and to compounds
and kits for use in such assays.

Almost one third of the carrot crop is lost
worldwide due to pests and diseases.

10 While chemical treatment of carrot growing fields
and of harvested carrots can be used to reduce the loss
in the carrot crop, this is expensive and means that the
carrots can not be sold as "organic".

15 There is thus a pressing need for a diagnostic
method with the use of which loss in crop yield may be
reduced.

Root vegetables like carrots are particularly
susceptible to pathogens present in the soil in which
they are grown and especially to fungal infection. Such
fungal infection can cause damage to the carrots while
20 still in the ground or the damage may occur later during
post-harvest storage.

One especially damaging fungal infection of carrots
is called cavity spot and is caused by fungi of the
species *Pythium*, especially *P. viola* and *P. sulcatum*.
25 This infection damages the surface of the carrot root
while it is still in the ground and renders the carrots
essentially worthless.

Fungal infection of carrot growing fields may, as
mentioned above, be treated by spraying the fields with
30 antifungal agents, e.g. metalaksyl. Alternatively the
infected fields may be used for other crops not
sensitive to fungal infection by *Pythium* species until
the infection has disappeared. However, waiting for the
infection to clear is a long and uncertain business as
35 the fungus may have other host species available and as
viable fungal spores can remain dormant in the soil for
years.

We have now found that soil from fields in which carrots might be grown may be analysed to determine whether the fields are infected with Pythium thus enabling the grower to decide whether to spray with an antifungal agent or to avoid planting such fields with carrots until a later season when the infection has disappeared.

Thus viewed from one aspect the invention provides an assay method for detecting fungal infection of soil by pathogenic Pythium species, said method comprising: obtaining a sample of soil; treating said sample to lyse fungal cells therein; using an oligonucleotide primer pair, effecting a polymerase chain reaction on DNA released by lysis of the fungal cells; and detecting DNA fragments generated by said polymerase chain reaction; wherein said primer pair comprises an 18- to 24-mer having the ability to hybridize to one of the oligonucleotide sequences of formulae Ia, Ib, IIa, IIb, IIIa, IIIb, IVa, IVb, Va, Vb, VIa, VIb, VIIa, VIIb, VIIIa, VIIIb, IXa, IXb, Xa and Xb:

	5' - TCA CTT GTG GGG TAA AGA AGA - 3'	(Ia)
	5' - AGA CCA CAA TAA AGC GGC - 3'	(Ib)
	5' - AGT CCC GCA CAC ACA CAT - 3'	(IIa)
25	5' - ACT TCT CTC TTT GGG GAG TGG - 3'	(IIb)
	5' - TTC GTT CAG CCT CTG CAT - 3'	(IIIa)
	5' - TCG TTT CGG CTA TGA ATA CAG - 3'	(IIIb)
	5' - ACA AAT ATA CCA ACC ACA GCG - 3'	(IVa)
	5' - TTT GTA CTT GTG CAA TTG GC - 3'	(IVb)
30	5' - AAC GAA TAT ACC AAC CGC TG - 3'	(Va)
	5' - TCA TCT ATT TGT GCA CTT CTT TTT - 3'	(Vb)
	5' - TCT TCT TTA CCC CAC AAG TGA - 3'	(VIa)
	5' - GCC GCT TTA TTG TGG TCT - 3'	(VIb)
	5' - ATG TGT GTG TGC GGG ACT - 3'	(VIIa)
35	5' - CCA CTC CCC AAA GAG AGA AGT - 3'	(VIIb)
	5' - ATG CAG AGG CTG AAC GAA - 3'	(VIIIa)
	5' - CTG TAT TCA TAG CCG AAA CGA - 3'	(VIIIb)

5' - CGC TGT GGT TGG TAT ATT TGT - 3' (IXa)
5' - GCC AAT TGC ACA AGT ACA AA - 3' (IXb)
5' - CAG CGG TTG GTA TAT TCG TT - 3' (Xa)
5' - AAA AAG AAG TGC ACA AAT AGA TGA - 3' (Xb).

5

In the assay method of the invention, the primer pair preferably comprises an 18- to 24-mer having the ability to hybridize to one of the oligonucleotide sequences of formulae Ia, Ib, IIa, IIb, IIIa, IIIb, IVa, IVb, Va and Vb. Even more preferably the primer pair comprises a pair of 18- to 24-mers having the ability to hybridize to a pair of the oligonucleotide sequences of formulae Ia and Ib, IIa and IIb, IIIa and IIIb, IVa and IVb or Va and Vb. Less preferably the second primer may be a general primer that binds to all or substantially all fungal DNA. Such general primers, typically also 18- to 24-mers, are known and will still allow the polymerase chain reaction to function efficiently. Indeed such general primers are known which hybridize to DNA of all fungi, all oomycetes and all plants.

Examples of such general primers include:

5' - TCC GTA GGT GAA CCT GCG G - 3' (A)
5' - GCT GCG TTC TTC ATC GAT GC - 3' (B)
25 5' - GCA TCG ATG AAG AAC GCA GC - 3' (C)
5' - TCC TCC GCT TAT TGA TAT GC - 3' (D)
5' - GGA AGT AAA AGT CGT AAC AAG G - 3' (E)

General printers (A) and (E) are especially useful for use with specific printers which hybridize to sequences of formulae VIa, VIIa, VIIIa, IXa and Xa or less preferably Ib, IIb, IIIb, IVb and Vb. General primer (D) is especially useful for use with specific primers which hybridize to sequences of formula VIb, VIIb, VIIIb, IXb and Xb or less preferably Ia, IIa and IIIa. General primer (C) is especially useful for use with specific primers which hybridize to sequences

35

of formula Ia, IIa and IIIa.

General primer (B) is especially useful for use with specific primers which hybridize to sequences of formula Ib, IIb, IIIb, IVb and Vb.

5 By "having the ability to hybridize to" is meant having the ability to anneal to DNA incorporating such a sequence at the site of that sequence under conditions under which primer annealing in the performance of a PCR reaction may be effected.

10 One primer is preferably a compound consisting of or comprising a sequence of formulae Ia, Ib, IIa, IIb, IIIa, IIIb, IVa, IVb, Va, Vb, VIa, VIb, VIIa, VIIb, VIIIa, VIIIb, IXa, IXb, Xa or Xb or a derivative thereof in which up to 5 nucleotide residues: are omitted or
15 replaced by different residues; or are inserted; or are omitted from or added to the 3' or 5' termini. In the case of such derivatives, preferably no more than one residue is omitted at a 3' terminus and no more than 3 at a 5' terminus, preferably no C residue is replaced by
20 an A residue, preferably no more than 3 C or G residues are replaced, preferably no more than one omission or insertion within the listed sequence occurs and preferably any extension at the 3' termini is
5'-CAACA-3', 5'-CCACC-3', 5'-TGCTG-3', 5'-ACAGG-3',
25 5'-CCGGC-3', 5'-TTTGC-3', 5'-AGACA-3', 5'-AGAAG-3',
5'-CGAGA-3', 5'-GTTTG-3', 5'-GGCGC-3', 5'-GCCGA-3',
5'-GGCTG-3', 5'-AGGCC-3', 5'-GGTCG-3', 5'-CCAAA-3',
5'-TTATG-3', 5'-AACAC-3', 5'-TATGC-3' or 5'-CAGAT-3' or a fragment from the 5' end thereof for Ia, Ib, IIa, IIb,
30 IIIa, IIIb, IVa, IVb, Va, Vb, VIa, VIb, VIIa, VIIb, VIIIa, VIIIb, IXa, IXb, Xa and Xb respectively. More preferably, in such derivatives, no more than 3 residues are replaced or omitted, and particularly no more than 2 C or G residues are replaced.

35 Preferably one of the primers is a compound consisting of or comprising a sequence of formula VIa, VIb, VIIa, VIIb, VIIIa, VIIIb, IXa, IXb, Xa or Xb or

such a derivative thereof. More preferably the primer pair comprises the two compounds consisting of or comprising a sequence of formula VIa and VIb, VIIa and VIIb, VIIIa and VIIIb, IXa and IXb or Xa and Xb or such derivatives thereof.

In alternative preferred derivatives, none of the C or G residues are replaced or omitted. In further preferred derivatives any replacement, omission or addition of nucleotides is made in the 5' portion of the primer sequence, e.g. in the 5' half of the primer sequence. Preferably 8 or more nucleotide residues, e.g. 8, 9 or 10 residues, at the 3' end of the primers are not altered.

Fragments of such derivatives which have the ability to hybridise to sequences of formula Ia, Ib, IIa, IIb, IIIa, IIIb, IVa, IVb, Va, Vb, VIa, VIb, VIIa, VIIb, VIIIa, VIIIb, IXa, IXb, Xa or Xb are also included.

"Substantially homologous" as used herein in connection with a nucleic acid sequence includes those sequences having a sequence homology or identity of approximately 60% or more, e.g. 70%, 75%, 80%, 85%, 90%, 95%, 98% or more, with a particular sequence and also functionally equivalent variants and related sequences modified by single or multiple base substitution, addition and/or deletion. By "functionally equivalent" in this sense is meant nucleotide sequences which have the ability to hybridise to sequences of formula Ia, Ib, IIa, IIb, IIIa, IIIb, IVa, IVb, Va, Vb, VIa, VIb, VIIa, VIIb, VIIIa, VIIIb, IXa, IXb, Xa or Xb in accordance with the definition above. Such functionally equivalent variants may include synthetic or modified nucleotide residues providing the hybridisation function of the primer is retained.

Sequences which "hybridise" as used herein in connection with the definition of derivative primers are those sequences which bind (hybridise) to a particular

DNA sequence under conditions of low or preferably high stringency. Such conditions are well known and documented in the art. For example such sequences may hybridise to a particular DNA sequence under non-
5 stringent conditions (e.g. 6 x SSC, 50% formamide at room temperature) and can be washed under conditions of low stringency (e.g. 2 x SSC, room temperature, more preferably 2 x SSC, 42 C) or conditions of higher stringency (e.g. 2 x SSC, 65 C) (where SSC = 0.15M NaCl,
10 0.015M sodium citrate, pH 7.2).

Generally speaking, sequences which hybridise under conditions of high stringency are included within the scope of the invention.

The 18 to 24-mer primers may be prepared by
15 conventional chemical techniques, e.g. solid state synthesis.

It is especially preferred that two primer pairs be used in the method of the invention, one pair comprising primers hybridizing to sequences of formulae Ia and/or
20 Ib (or less preferably VIa and/or VIb) and another comprising primers hybridizing to sequences of formulae IIa and/or IIb (or less preferably VIIa and/or VIIb), more preferably a further pair comprising primers hybridizing to sequences of formulae IIIa and/or IIIb
25 (or less preferably VIIIa and/or VIIIb) is also used, still more preferably a still further pair comprising primers hybridizing to sequences of formulae IVa and/or IVb (or less preferably IXa and/or IXb) is used, most preferably five pairs of primers hybridizing to
30 sequences of formulae Ia to Vb are used. The primer pairs of formulae Ia to Vb (or VIa to Xb) detect respectively infection by *P. sulcatum*, *P. viola* L, *P. intermedium*, *P. sylvaticum* and *P. violae*/*P. pareocandrum*.

35 Such use of two or more primer pairs may be simultaneous or, more preferably in separate PCR reactions on aliquots of the sample.

The primers are themselves novel compounds and form a further aspect of the invention.

Viewed from this aspect the invention provides an 18- to 24-mer oligonucleotide primer hybridizable to an oligonucleotide sequence selected from those of formulae Ia, Ib, IIa, IIb, IIIa, IIIb, IVa, IVb, Va, Vb, VIa, VIb, VIIa, VIIb, VIIIa, VIIIb, IXa, IXb, Xa and Xb

Viewed from a still further aspect the invention provides a primer composition comprising a pair of 18- to 24-mer oligonucleotide primers at least one of which is hybridizable to an oligonucleotide sequence of formula Ia, Ib, IIa, IIb, IIIa, IIIb, IVa, IVb, Va, Vb, VIa, VIb, VIIa, VIIb, VIIIa, VIIIb, IXa, IXb, Xa or Xb, optionally together with a carrier.

The composition of the invention preferably comprises a pair of 18- to 24-mer oligonucleotide primers hybridizable to the oligonucleotide sequences of formula Ia and Ib, IIa and IIb, IIIa and IIIb, IVa and IVb or Va and Vb, optionally two, three, four or five such pairs.

For the detection phase of the method of the invention, it is possible to use labelled primers, e.g. radiolabelled or labelled with a chromophore or fluorophore or an enzyme. Such labelled versions of the primers of the invention and compositions containing them form further aspects of the invention.

Viewed from a yet still further aspect the invention provides a kit for the performance of the assay method of the invention, said kit comprising at least one primer pair according to the invention together with instructions for the performance of the assay method. Advantageously the kit also comprises a DNA-polymerase, e.g. Taq-polymerase, and especially advantageously the kit includes a set of components (e.g. chemical compositions) for DNA extraction.

The soil sample, approximately 0.5g for each PCR reaction, is preferably taken from a larger sample, for

example at least 100g, more preferably at least 200g, e.g. up to 1000g, which has been mixed (e.g. by physical intermingling of the larger sample or by addition together of aliquots of different parts of the larger sample) so that the sample analysed is representative of the larger sample - this is in distinct contrast to conventional PCR-based DNA analysis of soil where such representative sampling is not effected. The sample may be taken from a single location or it may be the combination of samples from multiple locations in a growing area (e.g. a field). The separate analysis of multiple samples from different locations in a field is preferable but, for reasons of economy, analysis of a composite sample may be preferred.

The soil is preferably taken at a depth of up to 30 cm, especially 1 to 20 cm. Samples are also preferably taken from both the margins and the central section of the growing area, preferably at a distance of at least 3m from the edge of the growing area (e.g. from a hedge, ditch, fence, track, etc).

Where the field is already in use in vegetable, e.g. carrot, production, the soil samples are advantageously taken from the soil within 10 cm, more preferably within 5 cm of the growing vegetables. Particularly conveniently, vegetables are uprooted and the soil on the uprooted vegetables is used for the assay.

We have found that humus in the soil reduced the accuracy of the assay method of the invention and thus pathogen DNA extraction from the soil samples preferably involves the following steps:

- 1) contact a sample of about 0.1 to 1g, preferably about 0.5g, soil taken from a mixed sample of at least 100g, preferably at least 200g, soil with a fungal cell lysing agent;
- 2) centrifuge at least 10000xg for at least 10 minutes

- and collect the supernatant;
- 3) contact the supernatant with a particulate DNA-binding agent;
 - 4) centrifuge and collect the DNA-bearing particulate;
 - 5) suspend the particulate in an aqueous solution of a chaotropic agent (e.g. an aqueous guanidine thiocyanate solution), centrifuge and collect the DNA-bearing particulate;
 - 6) repeat step (5) at least once;
 - 7) suspend the particulate in aqueous salt/ethanol wash solution, centrifuge and collect the DNA-bearing particulate;
 - 8) repeat step (7) at least once;
 - 9) suspend the particulate in an aqueous solution of a DNA-release agent;
 - 10) centrifuge and collect the DNA-containing supernatant; and optionally
 - 11) resuspend the particulate in an aqueous solution of a DNA-release agent, centrifuge and collect and combine the supernatant.

As compared with DNA-from-soil extraction using the commercially available kit FastDNA SPIN Kit for Soil (available from Qbiogene Inc/Bio 101 of Carlsbad, California, USA), this DNA extraction procedure involves a significantly longer post-lysis centrifugation, and repeated rinsing of the DNA-bearing particulate. In general also significantly larger volumes of release agent to free the DNA from the binding matrix should be used. Nonetheless the resultant procedure is one which provides good results for the full range of soil types in which vegetables are grown. The prior art extraction techniques in comparison are very sensitive to the soil type under investigation.

Thus viewed from a further aspect the invention provides a process for the extraction of nucleic acid (e.g. DNA) from soil which process comprises:

- 1) contact a sample of about 0.1 to 1g, preferably about 0.5g, soil taken from a mixed sample of at least 100g, preferably at least 200g, soil with a fungal cell lysing agent (e.g. a ceramic and silica particulate);
- 2) centrifuge at least 10000xg for at least 10 minutes and collect the supernatant;
- 3) contact the supernatant with a particulate DNA-binding agent;
- 4) centrifuge and collect the DNA-bearing particulate;
- 5) suspend the particulate in an aqueous solution of a chaotropic agent (e.g. an aqueous guanidine thiocyanate solution), centrifuge and collect the DNA-bearing particulate;
- 6) repeat step (5) at least once;
- 7) suspend the particulate in aqueous salt/ethanol wash solution (generally with a water/ethanol volume ratio of about 1:10), centrifuge and collect the DNA-bearing particulate;
- 8) repeat step (7) at least once;
- 9) suspend the particulate in an aqueous solution of a DNA-release agent;
- 10) centrifuge and collect the DNA-containing supernatant; and optionally
- 11) resuspend the particulate in an aqueous solution of a DNA-release agent (e.g. DNase in pyrogen-free water), centrifuge and collect and combine the supernatant.

Viewed from a further aspect the invention provides a kit for nucleic acid (e.g. DNA) extraction from soil, which kit comprises:

- i) a fungal cell lysing agent;
- ii) a DNA-binding particulate;
- iii) an aqueous solution of a chaotropic agent (e.g. guanidine thiocyanate);

- iv) an aqueous solution of salt and ethanol; and
- v) an aqueous solution of a DNA-release agent;

5 together with instructions for the use of said kit
in the process of the invention.

Where the sample under analysis is of vegetable
tissue rather than soil, it is preferably surface
tissue, in particular root (or tuber) surface tissue.
Such a sample may be taken for example by peeling the
10 root (or tuber surface) optionally after washing, wiping
or rinsing to remove soil. Such samples may be taken at
any stage during growth or storage but will preferably
(for analysing for *Pythium* spp. involved in cavity spot)
be taken from 2 weeks after sowing up to harvesting,
15 more preferably 4 weeks after sowing up to harvesting.
Where, as is preferred, the vegetable is carrot, we have
found that unsaturated organic compounds in the carrot
root reduced the accuracy of the assay method of the
invention and thus pathogen DNA extraction from
20 vegetable tissue samples preferably involves the
following steps:

- i) contact at least 20 mg of dry powdered plant tissue
(preferably surface tissue such as peel) with at
25 least 5 μ L/mg dry tissue of an aqueous fungal cell
lysing agent;
- ii) incubate;
- iii) mix with at least 4.5 μ L/mg dry tissue of an
aqueous solution of a protein and polysaccharide
30 precipitating agent;
- iv) centrifuge and collect DNA-containing supernatant;
- v) filter;
- vi) contact DNA-containing filtrate with a DNA-binding
substrate and centrifuge;
- 35 vii) wash the DNA-carrying substrate with an aqueous
ethanolic solution, centrifuge and remove the
liquid phase;

- viii) repeat step (vii) at least once;
- ix) dry the DNA-carrying substrate; and
- x) contact the substrate with an aqueous solution of a DNA release agent, centrifuge and collect the DNA-containing supernatant.

As compared with DNA-from-plant-tissue extraction using the commercially available GenElute Plant Genomic DNA kit (available from Sigma), this DNA extraction procedure involves the use of dry powdered plant tissue, larger volumes of lysing and precipitation solutions and drying of the DNA-carrying substrate to remove ethanol. Nonetheless the procedure does provide significantly better results and thus viewed from a further aspect the invention provides a process for the extraction of pathogen DNA from host vegetable tissue, which process comprises:

- i) contact at least 20 mg of dry powdered plant tissue (preferably surface tissue such as peel) with at least 5 μ L/mg dry tissue of an aqueous fungal cell lysing agent;
- ii) incubate;
- iii) mix with at least 4.5 μ L/mg dry tissue of an aqueous solution of a protein and polysaccharide precipitating agent;
- iv) centrifuge and collect DNA-containing supernatant;
- v) filter;
- vi) contact DNA-containing filtrate with a DNA-binding substrate and centrifuge;
- vii) wash the DNA-carrying substrate with an aqueous ethanolic solution, centrifuge and remove the liquid phase;
- viii) repeat step (vii) at least once;
- ix) dry the DNA-carrying substrate; and
- x) contact the substrate with an aqueous solution of a DNA release agent, centrifuge and collect the DNA-

containing supernatant.

Viewed from a still further aspect the invention provides a kit for pathogen DNA extraction from host vegetable tissue, which kit comprises:

- a) a fungal cell lysing agent;
- b) an aqueous solution of a protein and polysaccharide precipitating solution;
- c) a DNA-binding substrate;
- d) an aqueous ethanolic wash solution; and
- e) an aqueous solution of a DNA release agent;

together with instructions for the use of said kit for pathogen DNA extraction from host vegetable tissue.

In these techniques, the fungal cell lysing agent may for example be an enzyme (e.g. L1393 or L1412 from Sigma) or a buffered surfactant (e.g. cetyltrimethylammonium bromide, N-lauroylsarcosine or sodium dodecyl sulphate). Alternatively, mechanical means such as grinding in liquid nitrogen, may be used.

Proteins, polysaccharides and nucleic acids can be separated in these techniques by different strategies. Thus proteins can be precipitated leaving the nucleic acid in solution, for example by adjusting the osmolality of the solution, e.g. by the addition of salts, generally high concentration salt solutions, for example 3M sodium acetate. Proteins can alternatively be extracted using organic solvents such as chloroform or phenol.

DNA extracted from the samples will typically be purified before being subjected to PCR using the primers of the invention. This can be effected in conventional fashion, e.g. chromatographically. Thus for example Micro Bio-Spin chromatography columns (available from BioRad, Hercules, California, USA) may be used together with insoluble polyvinylpolypyrrolidone powder (e.g.

P6755 from Sigma) to purify the DNA.

For the primer pair which hybridizes to the sequences of formula Ia and Ib, the amplified section of DNA is about 646 bp, for the pair which hybridizes to the sequences of formulae IIa and IIb, the amplified section of DNA is about 352 bp, for the pair which hybridizes to the sequences of formulae IIIa and IIIb, the amplified section of DNA is about 380 bp, for the pair which hybridizes to the sequences of formulae IVa and IVb, the amplified section of DNA is about 330 bp, and for the pair which hybridizes to the sequences of formulae Va and Vb, the amplified section of DNA is about 329 bp.

The PCR reaction itself can again be effected conventionally, e.g. using the primer pair, the four deoxynucleotide triphosphates and a heat stable DNA polymerase (e.g. Taq polymerase, available from Roche). Generally at least 25, more preferably 30 to 50, cycles of the PCR reaction will be sufficient.

The amplified DNA, if present, may then be detected by conventional techniques, e.g. gel separation or hybridization to labelled probes (for example radiolabelled or chromophore/fluorophore labelled probes). Where labelled probes are used, these may typically comprise labelled versions of one of the primer pair or labelled oligonucleotides able to hybridize specifically to the PCR-amplified fragment. In this embodiment, the PCR product is typically detected by a photodetector during PCR amplification or taken up by a porous substrate which is then treated with the labelled probe and rinsed, whereafter the signal from the probe retained on the substrate may be detected, e.g. photometrically or using a radiation detector. Where more than one primer pair is used in the PCR reaction, more than one probe will likewise be used and these may be labelled in the same or different fashion, e.g. using labels with different characteristic

absorption or emission energies or wavelengths.

The detection of the amplified DNA may be used to provide a qualitative, semi-quantitative or quantitative indication of the pathogen infestation of the soil sample, e.g. a value in cells per unit weight or an indication that the pathogen content of the soil is above or below a predetermined threshold value, e.g. boundary value for the decision to plant or not plant a particular vegetable crop or the decision to apply or not apply a fungicide.

In a particularly preferred embodiment of the method of the invention, aliquots of the soil sample are also tested in similar fashion for the presence of the fungal pathogens responsible for other vegetable root disease, e.g. ring rot (caused by *Phytophthora* species, in particular *P. megasperma*), liquorice rot (caused by *Mycocentrospora acerina*), crater rot (caused by *Fibularhizoctonia carotae*), grey mould (caused by *Botrytis cinerea*), Sclerotinia rot (caused by *Sclerotinia sclerotiorum*), Chalaropsis rot (caused by *Chalaropsis thielavioides*), and other diseases caused by *Alternaria dauci*, *Cercospora carotae* and *Rhizoctonia solani*. Of these, testing for one or both of *M. acerina* and *F. carotae* is the most important as these, while generally resulting in symptom-free carrots at harvest, can cause major crop loss on prolonged storage. Thus if either is detected the harvested crop should be consumed or processed (e.g. cooked, canned or bottled) within about 12 weeks of harvest, more preferably within about 4 weeks. For *M. acerina* the primer pair conveniently comprises a pair of 18- to 24-mers at least one of which has the ability to hybridize to one of the oligonucleotide sequences of formulae XIa, XIb, XIIa and XIIb:

5' - GTT TGA ATG GAG TCC GAC CG - 3' (XIa)

5' - CGG CGT ACT TGC TTC GGA GC - 3' (XIb)

5' - CGG TCG GAC TCC ATT CAA AC - 3' (XIIa)

5' - GCT CCG AAG CAA GTA CGC CG - 3' (XIIb)

For *F. carotae* the primer pair conveniently
5 comprises a pair of 18- to 24-mers at least one of which
has the ability to hybridize to one of the
oligonucleotide sequences of formulae XIIIa, XIIIb, XIVa
and XIVb:

10 5' - TGG GAT TAA CGG GCA GAG AC - 3' (XIIIa)

5' - TTT CGC ATT CGG AGG CTT GG - 3' (XIIIb)

5' - GTC TCT GCC CGT TAA TCC CA - 3' (XIVa)

5' - CCA AGC CTC CGA ATG CGA AA - 3' (XIVb).

15 The primer pairs used in this regard are thus
preferably a pair of compounds consisting of our
comprising sequences of formulae XIa and XIb or XIIa and
XIIb or XIIIa and XIIIb or XIVa and XIVb, especially
XIIa and XIIb and XIVa and XIVb or derivatives thereof
20 in which up to 5 nucleotide residues: are omitted or
replaced by different residues; or are inserted; or are
omitted from or added to the 3' or 5' termini. In the
case of such derivatives, preferably no more than one
residue is omitted at a 3' terminus and no more than 3
25 at a 5' terminus, preferably no C residue is replaced by
an A residue, preferably no more than 3 C or G residues
are replaced, preferably no more than one omission or
insertion within the listed sequence occurs and
preferably any extension at the 3' termini is
30 5'-GCGGG-3', 5'-GCAGC-3', 5'-GTGCA-3', 5'-ATTGT-3',
5'-CCTTT-3', 5'-GCTGC-3', 5'-ACCCA-3' or 5'-CAAAT-3' or
a fragment thereof from the 5' end thereof for XIa, XIb,
XIIIa, XIIIb, XIIa, XIIb, XIVa and XIVb respectively.
More preferably, in such derivatives, no more than 3
35 residues are replaced or omitted, and particularly no
more than 2 C or G residues are replaced.

As with the primers of formulae Ia to Xb, these

further primers can be prepared by conventional synthetic methods, in particular solid state synthesis.

The amplified DNA sequences produced using primer pairs XIIa and XIIb, and XIVa and XIVb are respectively
5 about 294 and 359 bp.

While the method of the invention is particularly suited for use on soil from fields in which carrots are to be grown or are growing, it is also more generally applicable to fields for vegetable (in particular root
10 vegetable) and potato production, especially parsnip, celery, lettuce, brassica and potato.

In place of the primers Ia to Xb it is possible to use in the method of the invention further primers which hybridize specifically to DNA of a *Pythium* species
15 selected from *Pythium violae*/P. *pareocandrum* like, P. *intermedium*, P. *sylvaticum*, P. *sulcatum*, P. *sulcatum* like and P. *viola* L. By specific hybridization it is meant that the primers are capable of being used to amplify DNA from the particular *Pythium* species in a PCR
20 reaction but not capable of being used to amplify DNA from a non-pathogenic *Pythium* species or carrot DNA. Typically, specificity may be tested for by checking against carrot DNA and DNA from the deposited *Pythium* strains P. *angustatum* CBS 676.95, P. *monospermum* CBS
25 790.95 and P. *connatum* CBS 678.95. The use of such primers in the method and kits of the invention in place of primers of formulae Ia to Xb is considered to fall within the scope of the present invention.

The invention will now be illustrated further by
30 the following non-limiting Examples.

Examples 1 to 10

Primers of formulae VIa to Xb

These were ordered by formula and prepared commercially
35 by Eurogentec, Serang, Belgium using conventional methods. Alternatively these may be prepared on a support matrix using a Pharmacia Gene Assembler Plus

instrument. The primers produced are then deprotected and cleared from the support matrix by overnight incubation at 55°C in 1 mL ammonia. Blocking groups and ammonia may be removed by chromatography on a Pharmacia
5 NAP 10 column with the primer being eluted in 1 mL water. Primer concentration can then be estimated spectrophotometrically using the factor $1 \text{ AU} = 20 \mu\text{g mL}^{-1}$ at 260 nm.

10 Example 11

DNA extraction from soil

A FastDNA SPIN kit for Soil (available from Qbiogene Inc /Bio 101) is used in this Example. A soil sample is collected and treated as follows:

- 15
1. Add 300 - 500 mg of soil to Multimix Tissue matrix Tube and place on ice. Process in FastPrep instrument for 20 seconds at speed 4.5 and place on ice. Add 980 μl Sodium Phosphate Buffer and 122 μl
20 MT Buffer and process in FastPrep instrument for 30 seconds at speed 5.5 and place on ice
 2. Centrifuge at 14,000 xg for 15 minutes and place on ice
 3. Transfer supernatant to new tubes (1.5 ml tubes) and add 250 μl PPS
25
 4. Mix by inverting the tubes by hand 10 times and centrifuge at 14,000 xg for 5 minutes
 5. Transfer supernatant to new tubes (2 ml tubes), add 1 ml RESUSPENDED Binding Matrix Suspension and
30 invert by hand for 2 minutes
 6. Centrifuge at 14,000 xg for 5 seconds and discharge supernatant
 7. Resuspend in 1 ml of 5.5M Guanidine Thiocyanate
 8. Centrifuge at 14,000 xg for 5 seconds and discharge
35 supernatant
 9. Resuspend in 600 μl of 5.5M Guanidine Thiocyanate and transfer to new tubes with Spin Filters

10. Centrifuge at 14,000 xg for 1 minute and empty catch tube
11. Add 500 μ l SEWS-M (aqueous salt/ethanol solution) to the Spin Filter (Wash 1) and resuspend matrix
- 5 12. Centrifuge at 14,000 xg for 1 minute and empty catch tube
13. Add 500 μ l SEWS-M to the Spin Filter (Wash 2) and resuspend matrix
14. Centrifuge at 14,000 xg for 1 minute and empty catch tube
- 10 15. Centrifuge 14,000 xg for 2 minutes
16. Place Spin Filters in new catch tubes and air dry for 5 minutes
17. Add 100 μ l DES and resuspend matrix
- 15 18. Centrifuge at 14,000 xg for 1 minutes
19. Store in fridge or at -20°C.

Example 12

DNA extraction from carrot peel

- 20 A GenElute Plant Genomic DNA kit (available from Sigma) is used in this Example. The carrot tissue sample is prepared by rinsing the carrot in water then peeling one third of the length of the top and tip. The peel is freeze dried then ground to powder. DNA extraction then
- 25 proceeds as follows:

1. Place about 50mg dried carrot tissue powder in a microfuge tube
2. Add 700 μ l of Lysis Solution Part A and 100 μ l of Lysis Solution Part B
- 30 3. Mix by vortexing and inversion and incubate at 65°C for 10 minutes with occasional inversions
4. Add 260 μ l Precipitation Solution and mix by inversions
- 35 5. Place on ice for 5 minutes
6. Centrifuge at 14,000 xg for 5 minutes (to pelletize cellular debris, proteins and polysaccharides)

7. Carefully transfer supernatant to a filtration column (BLUE filter in a collection tube)
8. Centrifuge at 14,000 xg for 1 minute and discard the filtration column
- 5 9. Add 700 μ l of Binding Solution and mix by pipetting up and down 3 times
- 10 10. Transfer about 700 μ l to a Nucleic Acid binding column (COLORLESS insert with a RED O-RING in a collection tube)
- 11 11. Centrifuge at 14,000 xg for 1 minute and empty the collection tube
- 12 12. Transfer the remainder of the liquid from step (9) to the Nucleic Acid binding column
- 13 13. Centrifuge at 14,000 xg for 1 minute and discard the collection tube
- 15 14. Place column in a new collection tube and add 500 μ l diluted Washing Solution (Wash 1)
- 15 15. Centrifuge at 14,000 xg for 1 minute and empty collection tube
- 20 16. Add 500 μ l diluted Washing Solution (Wash 2)
- 17 17. Centrifuge at 14,000 xg for 1 minute
- 18 18. Transfer column to new collection tube and air dry for 5 minutes
- 19 19. Elute DNA with 100 μ l pre-warmed (65°C) Elution solution by centrifugation at 14,000 xg for 1 minute.
- 25

Example 13

DNA Purification

- 30 For this Example, Micro Bio-Spin Chromatography columns (available from BioRad) and insoluble polyvinylpolypyrrolidone powder (P6755 from Sigma) are used. DNA purification is then effected as follows:
-

- 35 1. Place column in a 1.5 ml centrifuge tube
2. Fill column with polyvinylpolypyrrolidone powder to 1 mm below the edge and add 400 ml double distilled

H₂O

3. Centrifuge at 4,000 rpm (tabletop centrifuge) for 5 minutes
4. Transfer column to new 1.5 ml centrifuge tube and
5 add DNA extract from Example 11 or 12
5. Centrifuge at 4,000 rpm (tabletop centrifuge) for 4 minutes and discharge column
6. Store DNA at -20°C.

10 Examples 14 to 18

DNA amplification using the primers of Examples 1 to 10

The reactions are done in a total volume of 25 µl and the PCR reaction mixture is prepared as follows for the primers of Examples 1 to 8:

15

- | | |
|-----------|--|
| 15.87 µl | H ₂ O |
| 2.5 µl | 10 x PCR buffer containing 15 mM MgCl ₂ (Roche) |
| 2.0 µl | dNTP 2.5 mM |
| 2.5 µl | BSA (bovine serum albumin) 1 mg/ml |
| 20 0.5 µl | Forward primer (50 pmol/µl) |
| 0.5 µl | Reverse primer (50 pmol/µl) |
| 0.13 µl | Taq DNA polymerase (Roche) 5U/µl |
| 1.0 µl | DNA template |

- 25 For the primer pair of Examples 9 and 10, 14.37 µL H₂O is used, and 1.5 µL 25mM MgCl₂ is additionally used.

The PCR program used for the primers of Examples 1 to 6 is:

30

- | | | |
|-------|---------------------|--|
| 1. | Denaturation | 94°C 5 min |
| 2. | 30 cycles of | 94°C 20 sec, 60°C 30 sec, 72°C
30 sec |
| <hr/> | | |
| 3. | Terminal elongation | 72°C 2 min |
| 35 4. | Storage | 4°C |

The PCR program used for the primers of Examples 7 to 10

is:

1. Denaturation 94°C 5 min
2. 30 cycles of 94°C 30 sec, 56°C 30 sec,
5 72°C 30 sec
3. Terminal elongation 72°C 2 min
4. Storage 4°C

10 After amplification, 10 µl of the PCR product are added to 2 µl DNA loading buffer and run on a 1.2% agarose gel in 1 X TBE or 1 X TAE buffer at 100V for 45 minutes.

15 In Examples 14 to 18, the forward and reverse primers are the primers of formulae VIa and VIb of Examples 1 and 2, VIIa and VIIb of Examples 3 and 4, VIIIa and VIIIb of Examples 5 and 6, IXa and IXb of Examples 7 and 8 and Xa and Xb of Examples 9 and 10 respectively.

Example 19

20 Sensitivity

The primer pairs of Examples 1/2, 3/4, 5/6, 7/8, and 9/10 were tested against DNA extracted from *Pythium* intermedium, *Pythium sulcatum*, *Pythium sulcatum* like, *Pythium angustatum*, *Pythium aphanidermatum*, *Pythium*
25 *aquatile*, *Pythium coloratum*, *Pythium connatum*, *Pythium deliense*, *Pythium dissotocum*, *Pythium irregulare*, *Pythium mamilatum*, *Pythium middletonii*, *Pythium monospermum*, *Pythium myriotylum*, *Pythium rostratum*, *Pythium tracheiphilum*, *Pythium torulosum*, *Pythium*
30 *ultimum*, *Pythium* group F, *Pythium* group T, *Pythium* group HS, *Pythium sylvaticum*, *Pythium violae* L, *Pythium violae/Pythium pareocandrum* like, *Phytophthora infestans*, *Phytophthora cryptogea*, *Stemphyllium* sp.,
.....
Verticillium sp., *Fusarium* sp., *Rhizoctonia* sp.,
35 *Rhizoctonia solani*, *Cylindrocarpon* sp., *Botrytis* sp., healthy carrot, *Mycocentrospora acerina* and *Fibularhizoctonia carotea*.

The results are set out in Table 1 below.

Table 1

	Species	Example 1/2	Example 3/4	Example 5/6	Example 7/8	Example 9/10
5	Pythium intermedium	-	-	+	-	-
	Pythium sulcatum	+	-	-	-	-
10	Pythium sulcatum like	+	-	-	-	-
	Pythium angustatum	-	-	-	-	-
	Pythium aphanidermatum	-	-	-	-	-
15	Pythium aquatile	-	-	-	-	-
	Pythium coloratum	-	-	-	-	-
20	Pythium connatum	-	-	-	-	-
	Pythium deliense	-	-	-	-	-
	Pythium dissotocum	-	-	-	-	-
25	Pythium irregulare	-	-	-	-	-
	Pythium mamilatum	-	-	-	-	-
30	Pythium middletonii	-	-	-	-	-
	Pythium monospermum	-	-	-	-	-

	Pythium myriotylum	-	-	-	-	-
	Pythium rostratum	-	-	-	-	-
5	Pythium tracheiphilum	-	-	-	-	-
	Pythium torulosum	-	-	-	-	-
10	Pythium ultimum	-	-	-	-	-
	Pythium group F	-	-	-	-	-
	Pythium group T	-	-	-	-	-
15	Pythium group HS	-	-	-	-	-
	Pythium sylvaticum	-	-	-	+	-
20	Pythium violae L	-	+	-	-	-
	Pythium violae/ Pythium pareocandrum like	-	-	-	-	+
25	Phytophthora infestans	-	-	-	-	-
	Phytophthora cryptogea	-	-	-	-	-
30	Stemphyllium sp.	-	-	-	-	-
	Verticillium sp.	-	-	-	-	-
	Fusarium sp.	-	-	-	-	-

5	Rhizoctonia sp.	-	-	-	-	-
	Rhizoctonia solani	-	-	-	-	-
	Cylindrocarpon sp.	-	-	-	-	-
	Botrytis sp	-	-	-	-	-
	Healthy carrot	-	-	-	-	-
10	Mycocentrospor a acerina	-	-	-	-	-
	Fibularhizocto nia carotea	-	-	-	-	-

- = no DNA amplification

15 + = DNA amplification

Claims:

1. An assay method for detecting fungal infection of soil by pathogenic *Pythium* species, said method comprising:
- 5 obtaining a sample of soil; treating said sample to lyse fungal cells therein; using an oligonucleotide primer pair, effecting a polymerase chain reaction on DNA released by lysis of the fungal cells; and detecting DNA
- 10 fragments generated by said polymerase chain reaction; wherein said primer pair comprises an 18- to 24-mer having the ability to hybridize to one of the oligonucleotide sequences of formulae Ia, Ib, IIa, IIb, IIIa, IIIb, IVa, IVb, Va, Vb, VIa, VIb, VIIa, VIIb, VIIIa, VIIIb, IXa, IXb, Xa and Xb:
- 15

	5' - TCA CTT GTG GGG TAA AGA AGA - 3'	(Ia)
	5' - AGA CCA CAA TAA AGC GGC - 3'	(Ib)
	5' - AGT CCC GCA CAC ACA CAT - 3'	(IIa)
20	5' - ACT TCT CTC TTT GGG GAG TGG - 3'	(IIb)
	5' - TTC GTT CAG CCT CTG CAT - 3'	(IIIa)
	5' - TCG TTT CGG CTA TGA ATA CAG - 3'	(IIIb)
	5' - ACA AAT ATA CCA ACC ACA GCG - 3'	(IVa)
	5' - TTT GTA CTT GTG CAA TTG GC - 3'	(IVb)
25	5' - AAC GAA TAT ACC AAC CGC TG - 3'	(Va)
	5' - TCA TCT ATT TGT GCA CTT CTT TTT - 3'	(Vb)
	5' - TCT TCT TTA CCC CAC AAG TGA - 3'	(VIa)
	5' - GCC GCT TTA TTG TGG TCT - 3'	(VIb)
	5' - ATG TGT GTG TGC GGG ACT - 3'	(VIIa)
30	5' - CCA CTC CCC AAA GAG AGA AGT - 3'	(VIIb)
	5' - ATG CAG AGG CTG AAC GAA - 3'	(VIIIa)
	5' - CTG TAT TCA TAG CCG AAA CGA - 3'	(VIIIb)
	5' - CGC TGT GGT TGG TAT ATT TGT - 3'	(IXa)
	5' - GCC AAT TGC ACA AGT ACA AA - 3'	(IXb)
35	5' - CAG CGG TTG GTA TAT TCG TT - 3'	(Xa)
	5' - AAA AAG AAG TGC ACA AAT AGA TGA - 3'	(Xb)

2. A method as claimed in claim 1 wherein said primer pair comprises a pair of 18- to 24-mers having the ability to hybridize to a pair of the oligonucleotide sequences of formulae Ia and Ib or IIa and IIb or IIIa and IIIb or IVa and IVb or Va and Vb.

3. An 18- to 24-mer oligonucleotide primer hybridizable to an oligonucleotide sequence selected from those of formulae Ia, Ib, IIa, IIb, IIIa, IIIb, IVa, IVb, Va, Vb, VIA, VIB, VIIa, VIIB, VIIIA, VIIIB, IXa, IXb, Xa and Xb.

4. A primer composition comprising a pair of 18- to 24-mer oligonucleotide primers at least one of which is hybridizable to an oligonucleotide sequence of formula Ia, Ib, IIa, IIb, IIIa, IIIb, IVa, IVb, Va, Vb, VIA, VIB, VIIa, VIIB, VIIIA, VIIIB, IXa, IXb, Xa or Xb, optionally together with a carrier.

5. A kit for the performance of the assay method of claim 1, said kit comprising at least one primer pair as defined in claim 1 together with instructions for the performance of the assay method.

6. A process for the extraction of nucleic acid from soil which process comprises:

- 1) contact a sample of about 0.1 to 1g, preferably about 0.5g, soil taken from a mixed sample of at least 100g, preferably at least 200g, soil with a fungal cell lysing agent;
- 2) centrifuge at least 10000xg for at least 10 minutes and collect the supernatant;
- 3) contact the supernatant with a particulate DNA-binding agent;
- 4) centrifuge and collect the DNA-bearing particulate;
- 5) suspend the particulate in an aqueous solution of a

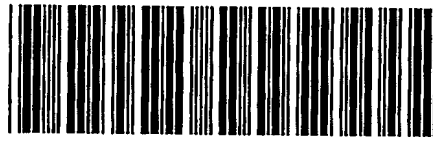
- chaotropic agent (e.g. aqueous guanidine thiocyanate solution), centrifuge and collect the DNA-bearing particulate;
- 5 6) repeat step (5) at least once;
- 7) suspend the particulate in aqueous salt/ethanol wash solution, centrifuge and collect the DNA-bearing particulate;
- 8) repeat step (7) at least once;
- 9) suspend the particulate in an aqueous solution of a DNA-release agent;
- 10 10) centrifuge and collect the DNA-containing supernatant; and optionally
- 11) resuspend the particulate in an aqueous solution of a DNA-release agent, centrifuge and collect and
- 15 combine the supernatant.

7. A kit for nucleic acid extraction from soil, which kit comprises:

- 20 i) an aqueous fungal cell lysing agent;
- ii) a DNA-binding particulate;
- iii) an aqueous solution of a chaotropic agent (e.g. guanidine thiocyanate);
- iv) an aqueous solution of salt and ethanol; and
- 25 v) an aqueous solution of a DNA-release agent;
- together with instructions for the use of said kit in the process of claim 5.

PCT Application

GB0304712



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